

SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: Ceriani, Roberto L.
Peterson, Jerry A.
Larocca, David J.
- (ii) TITLE OF THE INVENTION: FUSION PROTEIN WITH 46 KDALTON HMFG DIFFERENTIATION ANTIGEN BINDING SPECIFICITY, COMPOSITION, KIT & METHODS
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: V. Amzel & Assoc.
(B) STREET: P.O.Box 159
(C) CITY: Gladwyne
(D) STATE: Pennsylvania
(E) COUNTRY: USA
(F) ZIP: 19035
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk 3.5"
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
(D) SOFTWARE: PatentIn #1.0,
Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/482,596
(B) FILING DATE: June 7, 1995
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Amzel, Viviana
(B) REGISTRATION No.: 30,930
(C) REFERENCE/DOCKET No.:CRFC-047
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 610-649-0609
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(C) TELEX: N.A.

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:1384 base pairs
(B) TYPE:nucleic acid
(C) STRANDEDNESS:both
(D) TOPOLOGY:linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATTCATCC ATGATGTTAA TAAAAAACAC AAGGAGTTG TGGGTAAGT	50
GAACAAAAAC GCGGTGCATG TCAACCTGTT TGAGACCCCT GTGGAGGCTC	100
AGTACGTGAG ATTGTACCCC ACGAGCTGCC ACACGGCCTG CACTCTGCGC	150
TTTGAGCTAC TGGGCTGTGA GCTGAACGGA TGGCCAATC CCCTGGGCCT	200

GAAGAATAAC	AGCATCCCTG	ACAAGCAGAT	CACGGCCTCC	AGCAGCTACA	250
AGACCTGGGG	CTTGATCTC	TTCAGCTGGA	ACCCCTCCTA	TGCACGGCTG	300
GACAAGCAGG	GCAACTCAA	CGCCTGGGTT	GCGGGGAGCT	ACGGTAACGA	350
TCAGTGGCTG	CAGGTGGACC	TGGGCTCCTC	GAAGGAGGTG	ACAGGCATCA	400
TCACCCAGGG	GGCCCGTAAC	TTGGCTCTG	TCCAGTTGT	GGCATCCTAC	450
AAGGTTGCCT	ACAGTAATGA	CAGTGCACAC	TGGACTGAGT	ACCAGGACCC	500
CAGGACTGGC	AGCAGTAAGA	TCTTCCCTGG	CAACTGGGAC	AACCACCTCC	550
ACAAGAAGAA	CTTGTGAG	ACGCCCATCC	TGGCTCGCTA	TGTGCGCATC	600
CTGCCTGTAG	CCTGGCACAA	CCGCATCGCC	CTGCGCCTGG	AGCTGCTGGG	650
CTGTTAGTGG	CCACCTGCCA	CCCCCAGGTC	TTCCTGCTTT	CCATGGGCC	700
GCTGCCTCTT	GGCTTCTCAG	CCCCTTAAA	TCACCATAGG	GCTGGGACT	750
GGGGAAGGGG	AGGGTGTCA	GAGGCAGCAC	CACCAACACAG	TCACCCCTCC	800
CTCCCTCTT	CCCCCCTCC	ACCTCTCACG	GGCCCTGCCC	CAGCCCTAA	850
GCCCCGTCCC	CTAACCCCCA	GTCCTCACTG	TCCTGTTTC	TTAGGCACTG	900
AGGGATCTGA	GTAGGTCTGG	GATGGACAGG	AAAGGGCAAA	GTAGGGCGTG	950
TGGTTTCCCT	GCCCTGTCC	GGACCGCCGA	TCCCAGGTGC	GTGTGCTCT	1000
GTCTCTCTA	GCCCTCTCT	CACACATCAC	ATTCCCATGG	TGGCCTCAAG	1050
AAAGGCCCGG	AAGCCCCAGG	CTGGAGATAA	CAGCCTCTTG	CCC GTCGGCC	1100
CTGCGTCGGC	CCTGGGGTAC	CATGTGCCAC	AACTGCTGTG	GCCCCCTGTC	1150
CCCAAGACAC	TTCCCTTGT	CTCCCTGGTT	GCCTCTCTTG	CCC CTTGTCC	1200
TGAAGCCCAG	CGACACAGAA	GGGGGTGGGG	CGGGTCTATG	GGGAGAAAGG	1250
GAGCGAGGTC	AGAGGAGGGC	ATGGGTTGGC	AGGTGCGGCG	TTTGGGGCCC	1300
TCATGCTGGC	TTTTCACCCC	AGAGGACACA	GGCAGCTTCC	AAAATATATT	1350
TATCTTCTTC	ACGGGAAAAAA	AAAAAAAAAA	ACCG		1384

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp	Phe	Ile	His	Asp	Val	Asn	Lys	Lys	His	Lys	Glu	Phe	Val
1				5			10						
Gly	Asn	Trp	Asn	Lys	Asn	Ala	Val	His	Val	Asn	Leu	Phe	Glu
	15				20			25					
Thr	Pro	Val	Glu	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Thr	Ser
		30				35			40				
Cys	His	Thr	Ala	Cys	Thr	Leu	Arg	Phe	Glu	Leu	Leu	Gly	Cys
			45			50				55			
Glu	Leu	Asn	Gly	Cys	Ala	Asn	Pro	Leu	Gly	Leu	Lys	Asn	Asn
		60				65				70			
Ser	Ile	Pro	Asp	Lys	Gln	Ile	Thr	Ala	Ser	Ser	Ser	Tyr	Lys
			75				80						
Thr	Trp	Gly	Leu	His	Leu	Phe	Ser	Trp	Asn	Pro	Ser	Tyr	Ala
				85		90			95				
Arg	Leu	Asp	Lys	Gln	Gly	Asn	Phe	Asn	Ala	Trp	Val	Ala	Gly
		100				105			110				
Ser	Tyr	Gly	Asn	Asp	Gln	Trp	Leu	Gln	Val	Asp	Leu	Gly	Ser
			115				120			125			
Ser	Lys	Glu	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Arg	Asn
			130				135			140			
Phe	Gly	Ser	Val	Gln	Phe	Val	Ala	Ser	Tyr	Lys	Val	Ala	Tyr
				145			150						
Ser	Asn	Asp	Ser	Ala	Asn	Trp	Thr	Glu	Tyr	Gln	Asp	Pro	Arg
	155				160				165				
Thr	Gly	Ser	Ser	Lys	Ile	Phe	Pro	Gly	Asn	Trp	Asp	Asn	His
		170				175			180				
Ser	His	Lys	Lys	Asn	Leu	Phe	Glu	Thr	Pro	Ile	Leu	Ala	Arg
			185			190			195				
Tyr	Val	Arg	Ile	Leu	Pro	Val	Ala	Trp	His	Asn	Arg	Ile	Ala
		200				205			210				

Leu Arg Leu Glu Leu Leu Gly Cys
215

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val Gly
1 5 10
Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu Thr
15 20 25
Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser Cys
30 35 40
His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu
45 50 55
Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser
60 65 70
Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Tyr Lys Thr
75 80
Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg
85 90 95
Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly Ser
100 105 110
Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser Ser
115 120 120
Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn Phe
130 135 140
Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr Ser
145 150
Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg Thr
155 160 165
Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His Ser
170 175 180
His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr
185 190 195
Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala Leu
200 205 210
Arg Leu Glu Leu Leu Gly Cys
215 217

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Phe Lys Gly Asn Ser Thr Arg Asn Val Met Tyr Phe Asn Gly
1 5 10
Asn Ser Asp Ala Ser Thr Ile Lys Glu Asn Gln Phe Asp Pro
15 20 25
Pro Ile Val Ala Arg Tyr Ile Arg Ile Ser Pro Thr Arg Ala
30 35 40
Tyr Asn Arg Pro Thr Leu Arg Leu Glu Leu Gln Gly Cys Glu
45 50 55
Val Asn Gly Cys Ser Thr Pro Leu Gly Met Glu Asn Gly Lys
60 65 70
Ile Glu Asn Lys Gln Ile Thr Ala Ser Ser Phe Lys Lys Ser
75 80
Trp Trp Gly Asp Tyr Trp Glu Pro Phe Arg Ala Arg Leu Asn

85	90	95
Ala Gln Gly Arg Val Asn Ala Trp Gln Ala Lys Ala Asn Asn		
100	105	110
Asn Lys Gln Trp Leu Glu Ile Asp Leu Leu Lys Ile Lys Lys		
115	120	125
Ile Thr Ala Ile Ile Thr Gln Gly Cys Lys Ser Leu Ser Ser		
130	135	140
Glu Met Tyr Val Lys Ser Tyr Thr Ile His Tyr Ser Glu Gln		
145	150	
Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser Ser Met Val		
155	160	165
Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His Val		
170	175	180
Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg		
185	190	195
Val Ile Pro Lys Thr Trp Asn Gln Ser Ile Ala Leu Arg Leu		
200	205	210
Glu Leu Phe Gly Cys Asp Ile Tyr		
215	218	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly		
1	5	10
Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro		
15	20	25
Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr		
30	35	40
Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp		
45	50	55
Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala		
60	65	70
Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn		
75	80	
Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu		
85	90	95
Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro		
100	105	110
Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val		
115	120	125
Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Glu		
130	135	140
Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly		
145	150	
His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val		
155	160	165
Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser		
170	175	180
Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro		
185	190	195
Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu		
200	205	210
Gly Cys Glu Ala Gln Asp Leu Tyr		
215	218	